

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: January 9, 2002, 01:18:04 ; Search time: 10687.2. Seconds

**Title:** US-08-913-842-2  
**Perfect score:** 1965  
**Sequence:** 1 AAGCTTCAAGTAAAGTCCTG... TGAACACAAAGGAAATTC 100E

Scoring table: IDENTITY\_NUC  
GaPNT 10.0, Gapext 1.0  
searched: 17316

1 number of hits satisfying chosen parameters:  
minimum DB seq length: 0

Maximum DB seq length: 2000000000  
post-processing: Minimum Match 0%

Database : GenEmbl.\* Listing first 45 summaries

1: *gb*\_ba:  
2: *gb*\_htg:  
3: *gb*\_in:\*

卷之三

```
6: gb_pat;*
7: gb_ph;*
8: gb_pl;*
```

```
10: gb_ro:*
11: gb_sts:*
12: gb_err:*
```

13: gb\_un:\*

14: gb\_v1:\*

15: em\_ba:\*

```
17: em_hum:*
18: em_in:*
19: em_em:*
```

```
20: em_or:*
21: em_ov:*
22: em_pat:*
```

```
24: em_pl:*
25: em_ro:*
26: em_stor:*
```

27: em\_sy:\*

28: em\_un:\*

29: em\_vi:\*

```
31: em_htgo_inv: *
32: em_htgo_rod: *
33: em_htgo_hum: *
34: em_htg_inv: *
35: em_htg_rod: *
```

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Query Length	DB	ID	Description
1	178	9.1	1319	8	VIREXT5
2	115.6	5.9	136098	9	AC006970
3	114.8	5.8	12029	3	AE01422
4	114.6	5.8	86827	3	PPMAL3P5
5	112.4	5.7	136098	9	AC006970
6	112.2	5.7	259474	9	HDAC006970
7	112	5.7	196152	2	AC079795
8	111.6	5.7	158398	2	AC011146
9	110.2	5.6	86827	3	PPMAL3P5
10	110	5.6	161991	2	AC055860
11	109.6	5.6	158398	2	AC011146
12	109.2	5.6	115218	9	HS199A1
13	108.8	5.5	193302	2	AC021992
14	108.6	5.5	67970	3	PPMAL1P3
15	108.4	5.5	142239	2	AL379035
16	108.2	5.5	175223	9	AC004617
17	108	5.5	148673	3	AB001398
18	108	5.5	157176	2	AC084166
19	107.6	5.5	326924	2	AC093082
20	107.4	5.5	39347	9	AL13506
21	107.4	5.5	140455	2	AL356793
22	107.4	5.5	201312	2	AC067000
23	107.2	5.5	156133	2	AL593056
24	107	5.5	176174	9	AC074783
25	106.8	5.4	128603	2	AL356272
26	106.6	5.4	172805	9	AC066008
27	106.6	5.4	178087	9	AC050589
28	106.4	5.4	4601	3	DMU11584
29	106.4	5.4	19517	3	DMU37541
30	106.4	5.4	104992	2	AC005504
31	106.4	5.4	169546	2	AC001157
32	106.2	5.4	120029	2	HSJ202H10
33	106.2	5.4	199335	2	AC026655
34	106	5.4	106763	9	AP002091
35	105.8	5.4	205094	2	CNS01RHQ
36	105.6	5.4	142239	2	AL390835
37	105.6	5.4	194212	2	AC091448
38	105.4	5.4	36977	2	AC023104
39	105.4	5.4	67970	3	PPMAILP3
40	105.4	5.4	161286	2	AC025120
41	105.4	5.4	175223	9	AC004617
42	105.2	5.4	326924	2	AC004682
43	104.8	5.3	169794	2	AC004688
44	104.8	5.3	172666	2	AC06181
45	104.8	5.3	183385	2	AL589943

molecular grafting between matrix polysaccharides in plant cell walls	
J. Biol. Chem. 268 (34), 25364-25368 (1993)	
9406597 2 (bases 1 to 1319)	Nishitani, K.
Direct Submission	Submitted (17-JUN-1993) Kazuhiko Nishitani, Kagoshima University, College of Liberal Arts, Department of Biology; Kagoshima, Kagoshima 890, Japan (E-mail: nishitani@cla.kagoshima-u.ac.jp, Tel:0992-85-8938, Fax:0992-85-8946)
	Submitted (17-JUN-1993) to DDBJ by:
	Kazuhiko Nishitani
	Department of Biology
	College of Liberal Arts
	Kagoshima University
	Kagoshima 890
	Japan
	Phone: 0992-85-8938
	Fax: 0992-85-8946.
Location/Qualifiers	
1. 1319	
/organism="Vigna angularis"	
/db_xref="taxon:3914"	
/dev_stages="seedlings"	
176 .. 235	
/gene="ext"	
176 .. 1054	
/gene="ext"	
176 .. 1054	
/gene="ext"	
176 .. 1054	
/product="endo-xyloglucan transferase"	
/protein_id="BA01925.1"	
/db_xref="GI:469510"	
/translation="MGSSLWTCILLSIASASAFAANPRPPIDVPFGRNYVPTWAFDHT	
KYUNGSEIOLHLDKYTGFTGOSKGSYLFGHESMYIKVPGISAGTVTAFLSSTNAE	
HDEIDELRNGRKGPIVLPQIYDPTQHRISVLSWMMQIV	
FYVDDYPYRIVFKNSNDLGVKFPNQPMITYNSLWNADWATRGGLEKLSWMMQIVAS	
YKFFHIDGCEASYNAKFCDTQGRWMQDPERFDLDAQWQKLAWRNKTYTIVNCTDR	
399 a 276 c 261 g 383 t	
FEATURES	
source	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"	
Center project name: H_DJ0725G10.	
Location/Qualifiers	
1. 136098	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="RP4-725G10"</td	



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

on nucleic - nucleic search, using sw model  
Run on: January 8, 2002, 19:07:28 ; Search time 10687.2 seconds  
(without alignments) 2894.334 Million cell updates/sec

Title: US-08-913-842-1  
Perfect score: 1875  
Sequence: 1 AAGCTTTTGACATATTTG.....TGAACACACAAAGAAAATG 1875  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

1 number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*

- 1: gb\_ba:\*
- 2: gb\_htg:\*
- 3: gb\_in:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_phi:\*
- 8: gb\_pl:\*
- 9: gb\_p:\*
- 10: gb\_rc:\*
- 11: gb\_sts:\*
- 12: gb\_sv:\*
- 13: gb\_un:\*
- 14: gb\_vl:\*
- 15: em\_ba:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
- 19: em\_on:\*
- 20: em\_or:\*
- 21: em\_pat:\*
- 22: em\_ph:\*
- 23: em\_pl:\*
- 24: em\_ro:\*
- 25: em\_sts:\*
- 26: em\_sy:\*
- 28: em\_un:\*
- 29: em\_vl:\*
- 30: em\_htg\_hum:\*
- 31: em\_htg\_inv:\*
- 32: em\_htg\_rid:\*
- 33: em\_htg\_num:\*
- 34: em\_htg\_inv:\*
- 35: em\_htg\_rid:\*
- 36: em\_htg\_other:\*

Result No.	Score	Query Match Length	DB ID	Description
1	178	9.5	1319	VIREXT5
2	173.2	9.2	205094	CNS01RHO
3	159.4	8.5	86827	PFM013P5
4	156.6	8.4	15839	AC011146
5	155.4	8.3	4601	DM011584
6	155.4	8.3	19517	DM0137541
7	154.2	8.2	4601	DM011584
8	154.2	8.2	19517	DM0137541
9	153.4	8.2	14857	AE001398
10	153.6	8.1	156933	AC026839
11	151.4	8.1	183584	AC012492
12	151.2	8.1	14331	AC091214
13	150.4	8.0	14867	AE001398
14	150.4	8.0	67970	PFM013P3
15	149.2	8.0	176174	AC007483
16	148.6	7.9	67970	PFM013P3
17	147.6	7.9	104932	AC001249
18	147.6	7.9	169546	AC004157
19	146.6	7.8	86827	PFM013P5
20	144.8	7.7	104992	AC005504
21	144.8	7.7	16956	AC004157
22	143.6	7.7	158398	AC011146
23	141.8	7.6	175223	AC004617
24	141.2	7.5	32924	AC093082
25	138.6	7.4	172666	AC046181
26	138.4	7.4	36977	AC092304
27	138.2	7.4	173349	AL596253
28	137.8	7.3	188330	AC091742
29	137.8	7.3	218078	AC068138
30	136.6	7.3	176174	AC007483
31	136.6	7.3	26524	AC093082
32	136.6	7.3	199551	AC006281
33	134.8	7.2	195551	AC006281
34	134.6	7.2	188330	AC091742
35	133.6	7.1	105649	AC045219
36	133.4	7.1	36977	AC092304
37	133.4	7.1	106550	AC007708
38	132.8	7.1	173349	AL596253
39	132	7.0	136098	AC006970
40	131.2	7.0	172666	AC046181
41	130.8	7.0	181581	AC026621
42	130.4	7.0	259474	HPAC004605
43	128.6	6.9	14001	PRCOMP1B
44	128.6	6.9	106763	AP00091
45	128	6.8	142239	AL390835

#### ALIGNMENTS

RESULT	1	VIRTEXT5	VIRTEXT5	VANGULARIS	LOCUS	VANGULARIS	1319 bp	mRNA	PLN	01-FEB-2000
DEFINITION		DEFINITION	VANGULARIS	mRNA for endo-xyloglucan	ACCESSION	VANGULARIS		transferase, complete cds.		
KEYWORDS		KEYWORDS		endo-glycanotransferase; endo-xyloglucan	VERSION	D16458	1	transferase; extracellular		
SOURCE		SOURCE		protein; glycosylated protein; molecular				grafting between		
ORGANISM		ORGANISM		xyloglucan polymers; novel glycosyltransferase.				VIGNA VANGULARIS		
				VIGNA VANGULARIS seedlings cDNA to mRNA.						
				Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;						
				Rosidae; eurosids I; Fabales; Fabaceae; Papilioideae; Phaseoleae;						
				Vigna.						
REFERENCE	1 (bases 1 to 1319)	AUTHORS	Okaawa,K., Sato,Y., Nakagawa,T., Asada,K., Kato,I., Tomita,E. and	Nishitani,K.	TITLE	Molecular cloning and cDNA sequencing of endoxylglucan		transferase, a novel class of glycosyltransferase that mediates		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.